

# SEQUENCE LISTING

<110> Busfield, Samantha J.

<120> NOVEL MOLECULES OF THE  
HERPESVIRUS-ENTRY-MEDIATOR-RELATED  
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1

<150> US 09/146,950

<151> 1998-09-03

<160> 58

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<213> Homo sapiens

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<221> CDS

<222> (297)...(875)

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Met
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35 40 45
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50 55 60 65
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atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg	635
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100 105 110	
aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc	683
Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val	
115 120 125	
cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc	731
Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser	
130 135 140 145	
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Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu	
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Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu	
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gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac ctc	875
Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu	
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aga	acc	gac	gtc	ttg	agg	ctg	gtg	ctg	tat	ctc	acc	ttc	ctg	gga	gcc	96
Arg	Thr	Asp	Val	Leu	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala	
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ccc	tgc	tac	gcc	cca	gct	ctg	ccg	tcc	tgc	aag	gag	gac	gag	tac	cca	144
Pro	Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	
			35				40					45				
gtg	ggc	tcc	gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggg	tat	cgt	gtg	aag	192
Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	
	50					55					60					
gag	gcc	tgc	ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	240
Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	
65					70					75					80	

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Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	

caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	

agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	

gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	

agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	

gtg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	

gag gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac	576
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35 40 45	
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50 55 60	
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val	
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Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
85 90 95	
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
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 Pro Cys Tyr Ala Pro Ala  
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 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
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 Pro Cys Tyr Ala Pro Ala  
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 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
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 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
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 -5 1 5 10  
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
 15 20 25  
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro





ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag	488
Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu	
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ggc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc	536
Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly	
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acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa	584
Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln	
85 90 95	
atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg	632
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aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc	680
Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val	
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130 135 140 145	
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165 170 175	
gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga	872
Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly	
180 185 190	
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Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser	
195 200 205	
ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg	968
Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val	
210 215 220 225	
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Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser Val	
230 235 240	
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Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu Ala	
245 250 255	
ctg cag gcc cct ccg gac gtc acc acg gtg gcc gtg gag gag aca ata	1112
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Met Glu Pro  
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cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac 163  
Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp  
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gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc ccc tgc tac 211  
Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr  
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gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc 259  
Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser  
40 45 50

gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc	307
Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys	
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ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac	355
Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr	
70 75 80	
att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt	403
Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys	
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Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu	
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Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp	
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Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly	
135 140 145	
cag agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag	595
Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln	
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aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt	643
Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys	
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cag cac cag acc aat tgg cct aat cat atg tgt gaa aag aag aaa gcc	691
Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala	
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Lys Gly	
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 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
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 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
 30 35 40  
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
 45 50 55  
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
 60 65 70  
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
 75 80 85 90  
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
 95 100 105  
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
 110 115 120  
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
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 Lys Lys Ala Lys Gly  
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<400> 19

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 aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc 96  
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
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 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro

35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag			192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys			
50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca			240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro			
65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc			288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys			
85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc			336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser			
100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc			384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile			
115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc			432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser			
130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc			480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr			
145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg			528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu			
165	170	175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag			576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys			
180	185	190	
aag aaa gcc aag ggg			591
Lys Lys Ala Lys Gly			
195			

<210> 20  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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 20 25 30  
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His  
 35 40 45  
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala  
 50 55 60

Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val  
65 70 75 80  
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His  
85 90 95  
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val  
100 105 110  
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro  
115 120 125  
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln  
130 135 140  
Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly  
145 150 155

<210> 21  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)...(38)

<400> 21

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-20 -15 -10  
Pro Cys Tyr Ala Pro Ala  
-5

<210> 22  
<211> 114  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(114)

<400> 22

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Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
1 5 10 15  
aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30  
ccc tgc tac gcc cca gct 114  
Pro Cys Tyr Ala Pro Ala  
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<210> 23  
<211> 34  
<212> PRT  
<213> Homo sapiens

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<400> 23
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1          5          10          15
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
      20          25          30
Val Cys

<210> 24
<211> 42
<212> PRT
<213> Homo sapiens

<400> 24
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1          5          10          15
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
      20          25          30
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
      35          40

<210> 25
<211> 42
<212> PRT
<213> Homo sapiens

<400> 25
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1          5          10          15
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
      20          25          30
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
      35          40

<210> 26
<211> 105
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(105)

<400> 26
tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag      48
Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys
 1          5          10          15

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc      96
Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
      20          25          30

aca gtg tgt      105
Thr Val Cys
      35

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<210> 27  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 27

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 28  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 28

tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 29  
 <211> 2313  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (85)...(642)

<400> 29



60  
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159  
207  
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303  
351  
399  
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543  
591  
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692  
752  
812  
872  
932

gtcgacccac gcgccggct gagttcctct gctggagttc atcctgctag ctgggttccc	60
gagctgccgg tctgagcctg aggc atg gag cct cct gga gac tgg ggg cct	111
Met Glu Pro Pro Gly Asp Trp Gly Pro	
1 5	
cct ccc tgg aga tcc acc ccc aga acc gac gtc tgc agg ctg gtg ctg	159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu	
10 15 20 25	
tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc	207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
30 35 40	
tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc	255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
45 50 55	
agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca	303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
60 65 70	
gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc	351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
75 80 85	
cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg	399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu	
90 95 100 105	
cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc	447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys	
110 115 120	
agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg	495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala	
125 130 135	
tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga	543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly	
140 145 150	
ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc	591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr	
155 160 165	
ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag	639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys	
170 175 180 185	
gct tgaagggtccc accctgagcg gcaccctggg cacatgcctg cgtccaggag	692
Ala	
agctgcaggg ctgaagcctg tgtgccccag ataaccctt ccatgggccc agacaaagcc	752
tcatcagatc tgagcttctt ggaggctcag gatgggcctt cccagaagca ggcccagagg	812
gaggctgcct ccagatcccc tgtcccctgg ggctgtgggt gtccctgaat gtcagggccca	872
tgggagggcc cctgggcttc aggggttggg gaaagtgaac actctgctct ttgtccacct	932



Glu Glu Cys Gln His Gln Thr Lys Lys Ala  
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<210> 31  
<211> 558  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(558)

<400> 31

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1 5 10 15

aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30

ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144  
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro  
35 40 45

gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag 192  
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
50 55 60

gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca 240  
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
65 70 75 80

ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc 288  
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
85 90 95

caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc 336  
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
100 105 110

agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc 384  
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
115 120 125

gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc 432  
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
130 135 140

agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc 480  
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
145 150 155 160

ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg 528  
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
165 170 175

gag gaa tgt cag cac cag acc aaa aag gct  
 Glu Glu Cys Gln His Gln Thr Lys Lys Ala  
 180 185

<210> 32  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 32

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 20 25 30  
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His  
 35 40 45  
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala  
 50 55 60  
 Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val  
 65 70 75 80  
 Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His  
 85 90 95  
 Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val  
 100 105 110  
 Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro  
 115 120 125  
 Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln  
 130 135 140  
 Thr Lys Lys Ala  
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<210> 33  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 33

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 -35 -30 -25  
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 -20 -15 -10  
 Pro Cys Tyr Ala Pro Ala  
 -5

<210> 34  
 <211> 114  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(114)

<400> 34  
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48  
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
1 5 10 15  
aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30  
ccc tgc tac gcc cca gct 114  
Pro Cys Tyr Ala Pro Ala  
35

<210> 35  
<211> 34  
<212> PRT  
<213> Homo sapiens

<400> 35  
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys  
1 5 10 15  
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr  
20 25 30  
Val Cys

<210> 36  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 36  
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
1 5 10 15  
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
20 25 30  
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
35 40

<210> 37  
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<212> PRT  
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<400> 37  
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
1 5 10 15  
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20 25 30  
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
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<210> 38  
<211> 105  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(105)

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Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	
1			5					10						15		

tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	gcc	tgc	ggg	gag	ctg	acg	ggc	96
Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	
			20					25					30			

aca	gtg	tgt														105
Thr	Val	Cys														
			35													

<210> 39

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 39

tgc	cct	cca	ggc	acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	48
Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	
1			5					10						15		

ctg	cag	tgc	caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	96
Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	
			20					25					30			

aac	tgc	tcc	agg	aca	gag	aac	gcc	gtg	tgt							126
Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys							
			35				40									

<210> 40

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 40

tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	cag	gac	ggg	gac	cac	tgc	gcc	48
Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	Cys	Ala	
1			5					10						15		

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96  
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
20 25 30

gga ggc acc gag agt cag gac acc ctg tgt 126  
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
35 40

<210> 41  
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<212> DNA  
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<220>  
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<222> (103)...(933)

<400> 41

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Met Glu Pro Pro  
1

gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc 162  
Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val  
5 10 15 20

ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc 210  
Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala  
25 30 35

cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag 258  
Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu  
40 45 50

tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg 306  
Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly  
55 60 65

gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att 354  
Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile  
70 75 80

gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac 402  
Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp  
85 90 95 100

cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac 450  
Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn  
105 110 115

gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg 498  
Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly  
120 125 130

gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag 546

Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln		
		135					140					145					
agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt	cag	aac	594	
Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn		
	150					155					160						
tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	gaa	tgt	cag	642	
Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln		
	165				170					175					180		
cac	cag	acc	aag	tgc	agc	tgg	ctg	gtg	acg	aag	gcc	gga	gct	ggg	acc	690	
His	Gln	Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr		
			185						190					195			
agc	agc	tcc	cac	tgg	gta	tgg	tgg	ttt	ctc	tca	ggg	agc	ctc	gtc	atc	738	
Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile		
			200					205					210				
gtc	att	gtt	tgc	tcc	aca	gtt	ggc	cta	atc	ata	tgt	gtg	aaa	aga	aga	786	
Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	Lys	Arg	Arg		
		215					220					225					
aag	cca	agg	ggt	gat	gta	gtc	aag	gtg	atc	gtc	tcc	gtc	cag	gta	ttg	834	
Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	Gln	Val	Leu		
	230					235					240						
atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	cac	ctc	ccc	tct	882	
Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	His	Leu	Pro	Ser		
	245				250					255					260		
ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	ggg	ctc	cca	gtt	930	
Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	Gly	Leu	Pro	Val		
			265					270					275				
ctc	tgagggtcct	gagtcctttca	agtacagcca	cggtagctca	ggaaagaacc											983	
Leu																	
cacccccctca	aactgaaagc	agtaaaatga	acccgagaaac	ctggagtcct	agggggggcct	1043											
gagcaggcag	ggtctccacg	attcgtgtgc	tcacagcgga	aaagacagga	ggcagaaggt	1103											
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gagacaatac	cctcattcac	ggggaggagc	ccaaaccact	gacccacaga	ctctgcaccc	1223											
cgacgccaga	gatacctgga	gcgacggctg	ctgaaagagg	ctgtccacct	ggcgaaacca	1283											
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gagaggtggg	gcccctgctg	gggtagagct	ggggacgcca	cgtgccattc	ccatgggcca	1403											
gtgagggcct	ggggcctctg	ttctgctgtg	gcctgagctc	cccagagtcc	tgaggaggag	1463											
cgccagttgc	ccctcgctca	cagaccacac	acccagccct	cctggggccag	cccagagggc	1523											
ccttcagacc	ccagctgtct	gcgcgctctga	ctcttggtggc	ctcagcagga	caggccccgg	1583											
gcactgcctc	acagccaagg	ctggactggg	ttggctgcag	tgtggtgttt	agtggatacc	1643											
acatcggaag	tgattttcta	aattggattt	gaattcggct	cctgttttct	atttgtcatg	1703											
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 30 35 40  
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
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 60 65 70  
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
 75 80 85 90  
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
 95 100 105  
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
 110 115 120  
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
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 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala  
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 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys  
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 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser  
 190 195 200  
 Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Ser  
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 Gly Leu Pro Val Leu  
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aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc				96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	20	25	30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca				144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag				192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca				240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc				288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc				336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc				384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc				432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc				480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg				528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	165	170	175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc				576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	180	185	190	
gga gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg				624
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	195	200	205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt				672
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys	210	215	220	
gtg aaa aga aga aag cca agg ggt gat gta gtc aag gtg atc gtc tcc				720
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser	225	230	235	240

gtc	cag	gta	ttg	atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	768
Val	Gln	Val	Leu	Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	
			245					250							255	

cac	ctc	ccc	tct	ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	816
His	Leu	Pro	Ser	Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	
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Gly	Leu	Pro	Val	Leu												
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			20					25					30			
Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	
			35				40					45				
Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	
	50					55				60						
Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	
65					70				75					80		
Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	
			85						90					95		
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	
			100					105					110			
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro	
		115					120					125				
Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln	
	130					135					140					
Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr	Ser	Ser	
145					150					155					160	
Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile	Val	Ile	
			165					170						175		
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			180					185					190			
Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	Gln	Val	Leu	Ile	Leu	
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	210					215					220					
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<211> 34

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Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly  
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Thr Val Cys  
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1				5					10					15		

ctg	cag	tgc	caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	96
Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	
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aac	tgc	tcc	agg	aca	gag	aac	gcc	gtg	tgt							126
Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys							
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1				5					10					15		

gcg	tgc	cgc	gct	tac	gcc	acc	tcc	agc	ccg	ggc	cag	agg	gtg	cag	aag	96
Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	
			20					25					30			

gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt							126
Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys							
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5 10 15

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<210> 57

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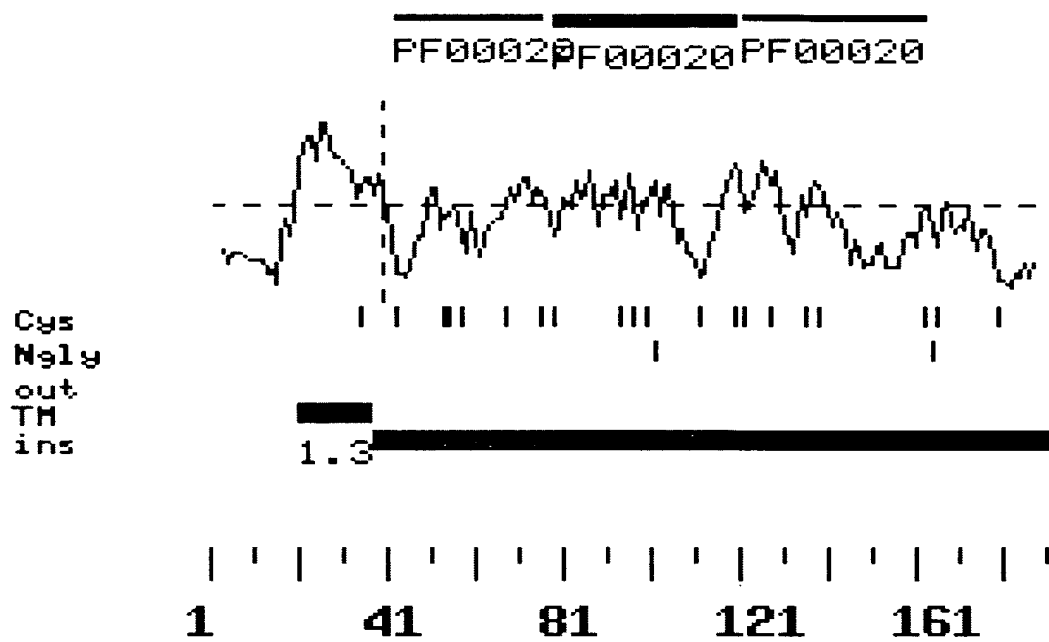
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Y L T F L G A P C Y A P A L P S C K E D 45
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E Y P V G S E C C P K C S P G Y R V K E 65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG 491
A C G E L T G T V C E P C P P G T Y I A 85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC 551
H L N G L S K C L Q C Q M C D P A M G L 105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG 611
A S R N C S R T E N A V C G C S P G H 125
GCG GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC 671
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TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC 731
G Q R V Q K G G T E S Q D T L C Q N C 165
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P P G T F S P N G T L E E C Q H Q T N R 185
GEC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA 851
W K S Q T D L * 194
GCT TGG AAA AGT CAG ACA GAC CTC TGA 878
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Figure 1



707280 684E660



*Figure 2*

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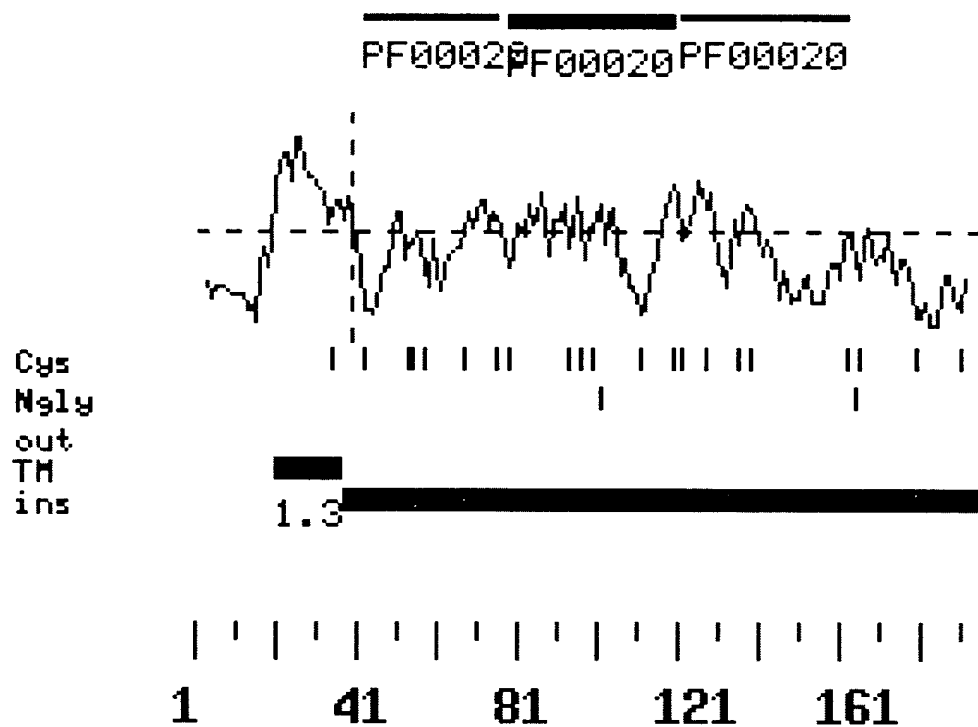
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S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
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C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
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C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA 325
V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT 385
L   Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG 445
E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   133
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CAG TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA 565
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K   A   K   G   *   198
AAA GCC AAG GGG TGA 700
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*Figure 3*

107230-6824200



*Figure 4*

**Figure 5**



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T P R T D V L R L V L Y L T F L G A P C	34
ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC	204
Y A P A L P S C K E D E Y P V G S E C C	54
TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC	264
P K C S P G Y R V K E A C G E L T G T V	74
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C E P C P P G T Y I A H L N G L S K C L	94
TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG	384
Q C Q M C D P A M G L R A S R N C S R T	114
CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA	444
E N A V C G C S P G H F C I V Q D G D H	134
GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC	504
A A C R A Y A T S S P G Q R V Q K G G	154
TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC	564
E S Q D T L C Q N C P P G T F S P N G	174
ACT GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG	624
L E E C Q H Q T K C S W L V T K A G A	194
ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC AGC TGG CTG GTG ACG AAG GCC GGA GCT	684
G T S S S H W V W W F L S G S L V I V I	214
GGG ACC AGC AGC TCC CAC TGG GTA TGG TGG TTT CTC TCA GGG AGC CTC GTC ATC GTC ATT	744
C S T V G L I I C V K R R K P R G D V	234
GTT TGC TCC ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT GTA	804
K V I V S V Q V L I L L P L S L P P P	254
GTC AAG GTG ATC GTC TCC GTC CAG GTA TTG ATC CTC CTC CCC CTC TCC CTC CCC CCT CCA	864
P S H L P S P R W G W C F W C T W W G L	274
CCT TCC CAC CTC CCC TCT CCC CGC TGG GGC TGG TGT TTC TGG TGT ACA TGG TGG GGG CTC	924
P V L *	278
CCA GTT CTC TGA	936
GGTCTGAGTCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCACCCCTCAAAGTCAAAGCAGTAAATGAAC	1015
CCGAGAACCTGGAGTCCCAGGGGGGCTGAGCAGGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGAAAAGACAGGAG	1094
GCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAATAC	1173
CCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCT	1252
GCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCTC	1331
CTCCAGTGGAGGGAGAGGTGGGGCCCTGTCTGGGGTAGAGCTGGGGACGCCACGTGCCATTTCCCATGGGCCAGTGAGGG	1410
CCTGGGGCTCTGTTCTGTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTTCGCTCACAGACC	1489
ACACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAG	1568
CAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACACAT	1647
CGGAAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGC	1726
TGTGGGAGGATGTAATATCTTGTTCCTCAAA	1805
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC	1834

Figure 7

PF00020 PF00020 PF00020

Cys  
Ngly  
out  
TH  
ins

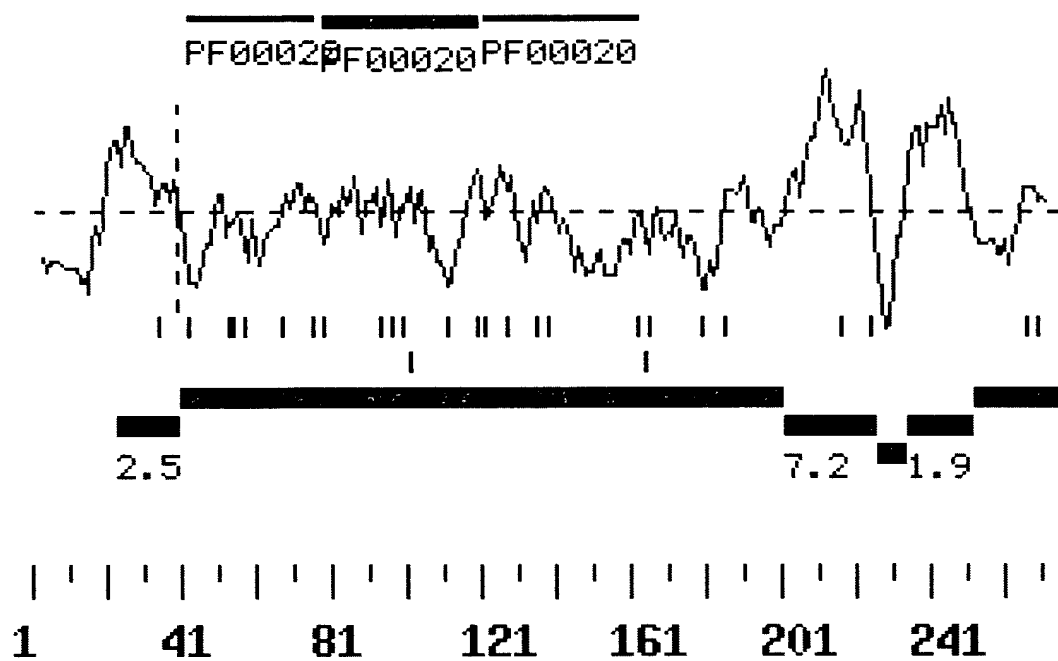


Figure 8

SHVEM_1_n.a.	1	80
SHVEM_2_n.a.	~GTCG-ACCCACGCGTCCGCTCGGCTTTGCTTGGACAGCTCCTGCCTCCCGCAGGGGCCACCTGTGTCCCCAGCGCCG	
SHVEM_3_n.a.	~GTCG-ACCCACGCGTCC-----GG-----ATG---A-----	
mHVEM_2_n.a.	~GTCG-ACCCACGCGTCC-----GC-----AC-----	
mHVEM__pub.__n.a.	CCTTCATACCGGCCCTTCCCTCGGCTTTGCTTGGACAGCTCCTGCCTCCCGCAGGGGCCACCTGTGTCCCCAGCGCCG	
SHVEM_1_n.a.	81	160
SHVEM_2_n.a.	CTCCACCCAGCAGGCCTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGTGCTCGGGTTCTGAGGC	
SHVEM_3_n.a.	-----AGGA-----	
mHVEM_2_n.a.	-----G-----	
mHVEM__pub.__n.a.	-----AG-----	
	CTCCACCCAGCAGGCCTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGTGCTCGGGTTCTGAGGC	
SHVEM_1_n.a.	161	240
SHVEM_2_n.a.	ACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCACAGCCGAGCAATGGCGCTGAGTT	
SHVEM_3_n.a.	-----CCGCAGCAATGGCGCTGAGTT	
mHVEM_2_n.a.	-----GCTGAGTT	
mHVEM__pub.__n.a.	-----CCGCAGCAATGGCGCTGAGTT	
	ACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCT-----CTTCTGGCCACAGCCGAGCAATGGCGCTGAGTT	
SHVEM_1_n.a.	241	320
SHVEM_2_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
SHVEM_3_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
mHVEM_2_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
mHVEM__pub.__n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
SHVEM_1_n.a.	321	400
SHVEM_2_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCCCTGGGAGCCCCCTG	
SHVEM_3_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCCCTGGGAGCCCCCTG	
mHVEM_2_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCCCTGGGAGCCCCCTG	
mHVEM__pub.__n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCCCTGGGAGCCCCCTG	
SHVEM_1_n.a.	401	480
SHVEM_2_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
SHVEM_3_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
mHVEM_2_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
mHVEM__pub.__n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
SHVEM_1_n.a.	481	560
SHVEM_2_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
SHVEM_3_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
mHVEM_2_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
mHVEM__pub.__n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
SHVEM_1_n.a.	561	640
SHVEM_2_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACCTGCTCCAGGAC	
SHVEM_3_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACCTGCTCCAGGAC	
mHVEM_2_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACCTGCTCCAGGAC	
mHVEM__pub.__n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACCTGCTCCAGGAC	
SHVEM_1_n.a.	641	720
SHVEM_2_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
SHVEM_3_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
mHVEM_2_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
mHVEM__pub.__n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
SHVEM_1_n.a.	721	800
SHVEM_2_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGCAAGTGCACCTGCCCCCG	
SHVEM_3_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGCAAGTGCACCTGCCCCCG	
mHVEM_2_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGCAAGTGCACCTGCCCCCG	
mHVEM__pub.__n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGCAAGTGCACCTGCCCCCG	

**Figure 9A**



SHVEM_1_n.a.	801	880
SHVEM_2_n.a.	GGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCAGCACCAGACCAAC-----	
SHVEM_3_n.a.	GGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCAGCACCAGACCAA-----	
mHVEM_2_n.a.	GGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCAGCACCAGACCAAAAAAGGCTTGAAGGTCCCACCCCTGAGCGGCA	
mHVEM_pub._n.a.	GGGACCTTCTCTCCCAATGGGACCCCTGGAGGAATGTCAGCACCAGACCAA-----	
SHVEM_1_n.a.	881	960
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	CCCTGGTCACATGCCCTGCGTCCAGGAGAGCTGCAGGGCTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCCAGAG	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	961	1040
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	CAAAGCCTCATCAGATCTGAGCTTCCCTGGAGGCTCAGGATGGGCCCTTCCCAGAAGCAGGCCAGAGGGAGGCTGCCTCCA	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1041	1120
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	GATCCCTGTCCCTTGGGGCTGTGGGTGTCCCTGAATGTCAGGGCCATGGGAGGGCCCTGGGCTTCAGGGGTGGGGAA	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1121	1200
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	AGTGAACACTCTGCTCTTGTCCACCTTCGGGAGGACACCTTCAAATGCTGACCCTGGGCCCCTAAGTACCTGAGACTT	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1201	1280
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	CAGAGCTTCTTGGGAGGAGCTGGGGTCCCCAGCGGAGCCTGGGATGGAGCAGGGATGGCTGCCCCAGGGAGGGGGCGGT	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1281	1360
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	GGGGCCTTCCATCCTGCTCTGCCCTCTCGTCCTCTGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTTTGT	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1361	1440
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	TCCCGACACTGGCTCTCCCTCTACCTTCTGTCCTTGTCTGCCACTGGTCTCCCGTGTCTGGGGTCTCTGCACTGCTGGC	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	
SHVEM_1_n.a.	1441	1520
SHVEM_2_n.a.	-----	
SHVEM_3_n.a.	TGCCTCCCGCTTCTCTCCCTCTCCCTCTGCCGTCTGTCTCCTTTGCCAGTCTCTCCTTGTTTCTCTTCTCCTCTCTC	
mHVEM_2_n.a.	-----	
mHVEM_pub._n.a.	-----	

**Figure 9B**

	1521		1600
shVEM_1_n.a.	-----CGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCC		
shVEM_2_n.a.			
shVEM_3_n.a.	CTTCTCTCCACCTCCCCATAGCCGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCC		
mHVEM_2_n.a.	-----		
mHVEM_pub._n.a.	-----		
	1601		1680
shVEM_1_n.a.	AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC		
shVEM_2_n.a.	-----		
shVEM_3_n.a.	AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC		
mHVEM_2_n.a.	-----G-----		
mHVEM_pub._n.a.	-----G-----		
	1681		1760
shVEM_1_n.a.	TGCACCTGCCTCTCCACGTCCTCGGCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
shVEM_2_n.a.	-----		
shVEM_3_n.a.	TGCACCTGCCTCTCCACGTCCTCGGCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
mHVEM_2_n.a.	-----TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
mHVEM_pub._n.a.	-----TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
	1761		1840
shVEM_1_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGGCTCCACAGTTGGCCTAATCATATG		
shVEM_2_n.a.	-----TTG-----GCCTAATCATATG		
shVEM_3_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGGCTCCACAGTTGGCCTAATCATATG		
mHVEM_2_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGGCTCCACAGTTGGCCTAATCATATG		
mHVEM_pub._n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGGCTCCACAGTTGGCCTAATCATATG		
	1841		1920
shVEM_1_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----		
shVEM_2_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGA-GCA--CACGG---CGGCCCCATCAGGG-----CTCATGTCCCCAGCCG		
shVEM_3_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
mHVEM_2_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
mHVEM_pub._n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
	1921		2000
shVEM_1_n.a.	-----		
shVEM_2_n.a.	TCACCTCTTGG-----AGCTCTG-TCACCCCAA---GCCTGG-----GAGGTGGC-CCCAGAGCTT		
shVEM_3_n.a.	-----		
mHVEM_2_n.a.	TCCCCCTCCACCTTCCACCTCCCCCTCTCCCCGCTGGGGCTGGTGTCTTCTGGTGACATGGTGGGGCTCCCAGTTCTC		
mHVEM_pub._n.a.	-----		
	2001		2080
shVEM_1_n.a.	-----		
shVEM_2_n.a.	TTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTG---CAGG-----CTGGG-GCAGG---		
shVEM_3_n.a.	-----		
mHVEM_2_n.a.	TG--AGGGTCCTGAG-TCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCACCCCTCAAAC TGAAAGCAGTAAAA		
mHVEM_pub._n.a.	-----		
	2081		2160
shVEM_1_n.a.	-----CAGCGGAAAAGACA		
shVEM_2_n.a.	TGA-----TG TAGTC--AAGG---TGATC-----G-TCTCCA-----TC-CAGCGGAAAAGACA		
shVEM_3_n.a.	-----CAGCGGAAAAGACA		
mHVEM_2_n.a.	TGAACCCGAGAACCTGGAGTCCCAGGGGGCCCTGAGCAGGCAGGGTCTCCACGATTCTGTGCTCAGCAGCGGAAAAGACA		
mHVEM_pub._n.a.	-----CAGCGGAAAAGACA		
	2161		2240
shVEM_1_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_2_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_3_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
mHVEM_2_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
mHVEM_pub._n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		

**Figure 9C**

shVEM_1_n.a.	2241	2320
shVEM_2_n.a.	TACCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_3_n.a.	TACCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM_2_n.a.	TACCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM__pub.__n.a.	TACCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_1_n.a.	2321	2400
shVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_3_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM__pub.__n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_1_n.a.	2401	2480
shVEM_2_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_3_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM_2_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM__pub.__n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_1_n.a.	2481	2560
shVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_3_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM__pub.__n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_1_n.a.	2561	2640
shVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_3_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM__pub.__n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_1_n.a.	2641	2720
shVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
shVEM_3_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
mHVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
mHVEM__pub.__n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
shVEM_1_n.a.	2721	2800
shVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
shVEM_3_n.a.	AAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
mHVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
mHVEM__pub.__n.a.	AAGTGATTTTCTAAATTGGATTGAATTCGGCTCCTGTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
shVEM_1_n.a.	2801	2880
shVEM_2_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
shVEM_3_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
mHVEM_2_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
mHVEM__pub.__n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
shVEM_1_n.a.	2881	2904
shVEM_2_n.a.	-----	
shVEM_3_n.a.	-----GGGCGGCCGC	
mHVEM_2_n.a.	AAAAAAAAAAAAAAGGGCGGCCGC	
mHVEM__pub.__n.a.	-----	

Figure 9D

	1	80
shVEM_1_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_2_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_3_a.a.	MEPPGDWGGPPWRSTPRTDVSRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM_2_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM__pub.__a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
	81	160
shVEM_1_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_2_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_3_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM_2_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM__pub.__a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
	161	240
shVEM_1_a.a.	LCQNCPPGTFSPNGTLEECQHQTNRWKSQTDL-----	
shVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTNPWPNHMCCKKAKG-----	
shVEM_3_a.a.	LCQNCPPGTFSPNGTLEECQHQTCKA-----	
mHVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHWVWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
mHVEM__pub.__a.a.	LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHWVWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
	241	283
shVEM_1_a.a.	-----	
shVEM_2_a.a.	-----	
shVEM_3_a.a.	-----	
mHVEM_2_a.a.	VQVLILLPLSLPPPPSHLPSRWGWCFWCTWWGLPVL-----	
mHVEM__pub.__a.a.	VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH	

Figure 10